OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: March 3, 2005, 21:55:55 ; Search time 693.243 Seconds
                                        (without alignments)
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Searched: 5401638 seqs, 296923429 residues

Total number of hits satisfying chosen parameters: 10803276

Post-processing: Minimum Match 0%
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Listing first 45 summaries

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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5	92.8	7.0	3325	19	US-10-741-600-701	Sequence 701, App
6	92.8	7.0	3289	19	US-10-741-600-702	Sequence 702, App
7	92.8	7.0	3677	19	US-10-741-600-699	Sequence 699, App
8	92.8	7.0	3821	19	US-10-741-600-700	Sequence 700, App
9	92.8	7.0	3979	19	US-10-741-600-704	Sequence 704, App
10	92.8	7.0	4083	19	US-10-741-600-703	Sequence 703, App
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c	15	60.2	4.5	604	13	US-10-027-632-57637	Sequence 57637, A
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c	19	59.8	4.5	353	18	US-10-674-124A-6831	Sequence 6831, Ap
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c	21	59.4	4.5	760	18	US-10-363-345A-4954	Sequence 4954, Ap
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c	23	58.8	4.4	233060	13	US-10-087-192-97	Sequence 97, Appl
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c	25	58.2	4.4	253	18	US-10-674-124A-18874	Sequence 18874, A
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c	27	58	4.4	122	18	US-10-674-124A-21464	Sequence 21464, A
c	28	58	4.4	150351	18	US-10-322-281-453	Sequence 453, App
c	29	57.6	4.3	1196	17	US-10-369-493-28676	Sequence 28676, A
c	30	57.6	4.3	65253	17	US-10-085-117-331	Sequence 331, App
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c	32	57.4	4.3	90650	14	US-10-175-523-80	Sequence 80, Appl
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c	39	57	4.3	84826	13	US-10-087-192-1561	Sequence 1561, Ap
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c	41	56.8	4.3	434	19	US-10-643-775-740	Sequence 740, App
c	42	56.8	4.3	609	19	US-10-723-860-631	Sequence 1057, Ap
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c	44	56.6	4.3	216	18	US-10-674-124A-26426	Sequence 26426, A
c	45	56.6	4.3	1258	13	US-10-027-632-123939	Sequence 123939,

ALIGNMENTS

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Sequence 17759, Application US/10741600

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Qy      284 CTACCATAAGCC----AGACTTATTTGTTCAGATGGGAGCAGCCTTCCCCCTCTGTGGGTAAG-- 338
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OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: March 3, 2005, 12:39:24 ; Search time 210.34 Seconds
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Perfect score: 1330
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	58	4.4	137226	4	US-09-949-016-13763	Sequence 13763, A
6	57.4	4.3	49301	4	US-09-949-016-16296	Sequence 16296, A
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26	56	4.2	66933	4	US-09-544-398B-11	Sequence 11, Appl
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ALIGNMENTS

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; Sequence 77451, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 77451
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-77451

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Best Local Similarity 81.9%;
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; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: March 3, 2005, 21:55:55 ; Search time 3172.76 Seconds
(without alignment)
11384.206 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 5401638 seqs, 296923429 residues
Total number of hits satisfying chosen parameters: 10803276

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	2637.4	43.3	5960	10	US-09-326-885-14	Sequence 14, Appl
6	2634.8	43.3	18116	10	US-10-790-455-7	Sequence 7, Appli
7	2634.8	43.3	18116	18	US-10-811-136B-7	Sequence 7, Appli
8	2634.8	43.3	18116	19	US-10-940-315-7	Sequence 7, Appli
9	2634.8	43.3	3327	18	US-10-796-486-56	Sequence 56, Appl
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13	2633.4	43.3	3976	18	US-10-796-486-49	Sequence 49, Appl1
14	2633.4	43.3	5163	18	US-10-796-486-54	Sequence 54, Appl1
15	2633.4	43.3	5283	18	US-10-796-486-58	Sequence 58, Appl1
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18	2632.8	43.3	5041	19	US-10-811-136B-6	Sequence 6, Appl1
19	2632.8	43.3	5041	18	US-10-940-315-6	Sequence 6, Appl1
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22	2632.8	43.3	5043	18	US-10-790-455-5	Sequence 5, Appl1
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44	2460	40.4	4516	9	US-09-968-355-24	Sequence 24, Appl1
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ALIGNMENTS

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RESULT 1
US-09-990-249A-2

; Sequence 2, Application US/0990249A
; Patent No. US2002010411A1
; GENERAL INFORMATION:
; APPLICANT: Chiu, Ing-Ming
; TITLE OF INVENTION: Transgenic animals for screening therapeutic agents for brain t[...
; FILE REFERENCE: 28489/04000
; CURRENT APPLICATION NUMBER: US/09/990,249A
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/252745
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.1
;
; SEQ ID NO 2
; LENGTH: 6087
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleotides 1-594, human FGF1B promoter; 595-3233, SV40; 3234-6[...]
; OTHER INFORMATION: 7, PGL2-Basic plasmid vector (Promega)
US-09-990-249A-2

  Query Match       100.0%;  Score 6087;  DB 9;  Length 6087;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 6087;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Db     61 ACCTGCTGTTTCCCTGGCGAACTCAGGCCTCAAAATAAACAGGATTCTGCTCAGACGCGGCC 120
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OM nucleic - nucleic search, using sw model

GenCore version 5.1.6

Run on: March 3, 2005, 12:39:24 ; Search time 962.66 Seconds (without alignments) 10346.346 Million cell updates/sec

Title: 6087
Perfect score: 6087
Sequence: 1 cccgggaggtcccttcatc.........ctgtaactgagctaacataa 6087
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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	1	3096	50.9	5789	3	US-08-862-431-32	Sequence 32, Appl
	2	3096	50.9	5791	3	US-08-862-431-31	Sequence 31, Appl
	3	3096	50.9	5793	3	US-08-862-431-30	Sequence 30, Appl
	4	3096	50.9	5793	3	US-08-862-431-29	Sequence 29, Appl
c		3096	50.9	5818	2	US-08-536-559A-3	Sequence 3, Appl
	5	3096	50.9	5819	2	US-08-536-559A-2	Sequence 2, Appl
	6	3096	50.9	5819	2	US-08-862-431-28	Sequence 28, Appl
	7	3096	50.9	5819	2	US-08-862-431-27	Sequence 27, Appl
	8	3096	50.9	5938	2	US-08-536-559A-4	Sequence 4, Appl
	9	3096	50.9	5938	2	US-08-862-431-26	Sequence 26, Appl
	10	3096	50.9	6092	3	US-08-536-559A-1	Sequence 1, Appl
	11	3096	50.9	6092	2	US-08-862-431-26	Sequence 26, Appl
	12	3091.2	50.8	10504	3	US-09-423-744A-19	Sequence 19, Appl
	13	2851.2	46.8	12143	3	US-09-423-744A-1	Sequence 1, Appl
	14	2647	43.5	5183	3	US-09-039-555B-18	Sequence 18, Appl
c	15	2645.4	43.5	5243	2	US-08-414-335-2	Sequence 2, Appli
	16	2633.4	43.3	3327	4	US-09-628-730-56	Sequence 56, Appl
	17	2633.4	43.3	3369	4	US-09-628-730-48	Sequence 48, Appl
	18	2633.4	43.3	3954	4	US-09-628-730-53	Sequence 53, Appl
	19	2633.4	43.3	3954	4	US-09-628-730-57	Sequence 57, Appl
	20	2633.4	43.3	3976	4	US-09-628-730-49	Sequence 49, Appl
	21	2633.4	43.3	5163	4	US-09-628-730-54	Sequence 54, Appl
	22	2633.4	43.3	5283	4	US-09-628-730-58	Sequence 58, Appl
	23	2633.4	43.3	5325	4	US-09-628-730-50	Sequence 50, Appl
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c	25	2468	40.5	2479	3	US-09-359-081-4	Sequence 4, Appli
c	26	2459	40.4	2479	3	US-09-232-463-8	Sequence 8, Appli
c	27	2459	40.4	3656	1	US-09-232-463-9	Sequence 9, Appli
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c	41	2455.2	40.3	9454	1	US-08-232-463-3	Sequence 3, Appli
c	42	2455.2	40.3	9454	1	US-08-232-463-4	Sequence 4, Appli
c	43	2449.8	40.2	6601	1	US-08-232-463-15	Sequence 15, Appli
c	44	2449.8	40.2	7218	1	US-08-232-463-14	Sequence 14, Appli
c	45	2449.8	40.2	9890	1	US-08-232-463-18	Sequence 18, Appli

ALIGNMENTS

RESULT 1
US-08-862-431-32
; Sequence 32, Application US/08862431
; Patent No. 6120994
; GENERAL INFORMATION:
; APPLICANT: TAM, SHUI-PANG
; TITLE OF INVENTION: ANTIOXIDANT RESPONSIVE ELEMENT
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862,431
; FILING DATE: 23-MAY-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kim, Judith U.
; REGISTRATION NUMBER: 40,679
; REFERENCE/DOCKET NUMBER: 1669.0020000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
US-08-862-431-32

Query Match 50.9%; Score 3096; DB 3; Length 5789;
Best Local Similarity 100.0%;
Matches 3096; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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